

MDQSSRRDESYHETHPGSLDPSHQSHPHPHPTLHRPNQGGVYDSPQH 50
GMFQQPYQQHGGFHQQNELQHLREFSDSHDNAFSSHSYQQDRAGVSTLPN 100
NISHAYGSGHPLAESQHSGGPGSGPRIDPNHHHPHQDDPHRPSEPLSHPSS 150
TGSHQGTTHQQYHERSHHLNPQQNRDHADTISYRSSTRFYRSHAPFSRQE 200
RPHLHADHHHGHHAHSHHGEHPHHKEQRHYHGDHMHIIHHRSPSASQL 250
SHKSHSTLATSPSHVGSKSTASGARYTFGARSQIFGKAQSRESLRESASL 300
SEGEDHVQKRKKAQRAHKKHAHTGNIFQLLWEKISHLLGLQQMILSLTQS 350
S1 S2
LGFETFI FIVVCLNTVILVAQT FTELEIRGEWYFMVLDSIFLSIYVLEAV 400
S3
LKLIALGLEIFYFDPWNNLDFFIMVMAVLDFVLLQINSLSYSFYNHSLFRI 450
S4 S5
LKVFKSMRALRAIRVLRRLSILTSLHEVAGTLSGSLPSITAILTLMFTCL 500
P
FLFSVVLRALFQDSDPKRFQNIFFTTLFTLTMLTLDWLSLIYIDNRAQGA 550
S6
WYIIPILMIYIVIQYFIFLNLVIAVLVDNFMQALLKGLEKVKLEQAARVH 600
EKLLDSDLTDLNKADANAQMTTEALKMQLIEGMFGNMTVKQRVLFHFQFLQ 650
LVAAVEHQHQKFRSQAYVIDELVDMAFEAGDDDDYGK 686

FIG. 1A

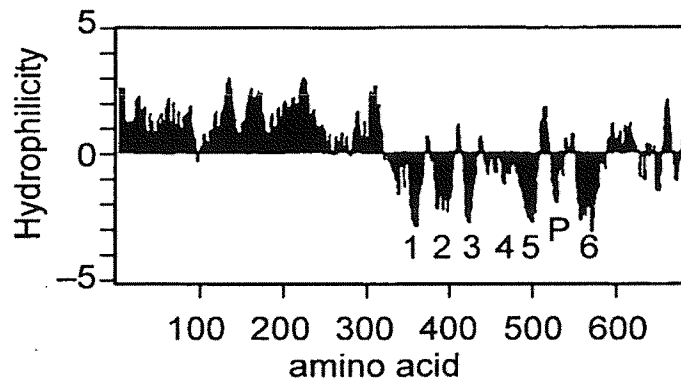


FIG. 1B

Pore region	
CatSper	RFQNI FTTLFTLFTMLTLD DWSLIYID
Cav1.2	NFDNFAFAMLT V FQCI TMEGWTDVLYN
I Cav2.2	NFDNILFAILT V FQCI TMEGWTDILYN
Cav3.1	NFDNIGYAWIAIFQVITLEGWVDIMYF
Cav1.2	TFDNFPQSLLTVFQILTGEDWNSVMYD
II Cav2.2	NFDTFPAAILTVFQILTGEDWNAVMYN
Cav3.1	NFDSLLWAI V TVFQILTQEDWNKVLYN
Cav1.2	DFDNVLAAMMAFTVSTFEGWPPELLYR
III Cav2.2	HYDNVLWALLTFTVSTGEGWPMYLKH
Cav3.1	NFDNLGQALMSLFVLASKDGWVDIMYD
Cav1.2	NFQTFPQAVLLLPRCATGEAWQDIMLA
IV Cav2.2	NFRTFLQALMLLFRSATGEAWHEIMLS
Cav3.1	TFRNFGMAFLTFRVSTGDNWNGIMKD

FIG. 1C

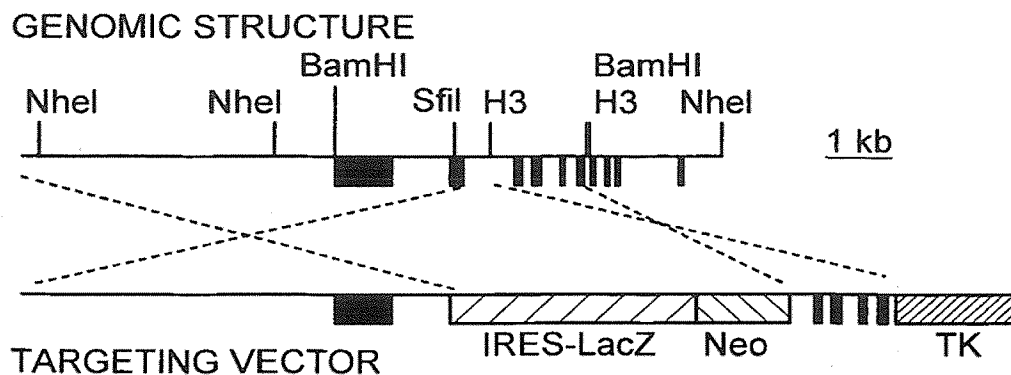


FIG. 2

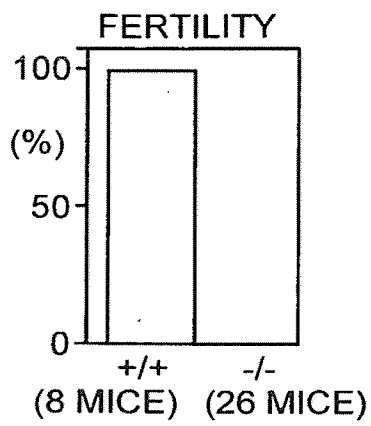


FIG. 3A

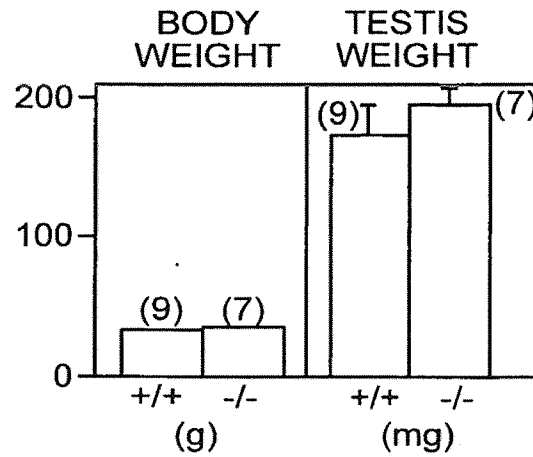


FIG. 3B

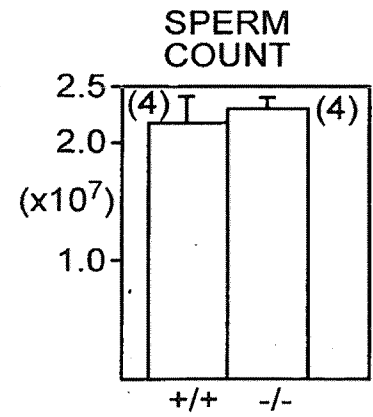


FIG. 3C

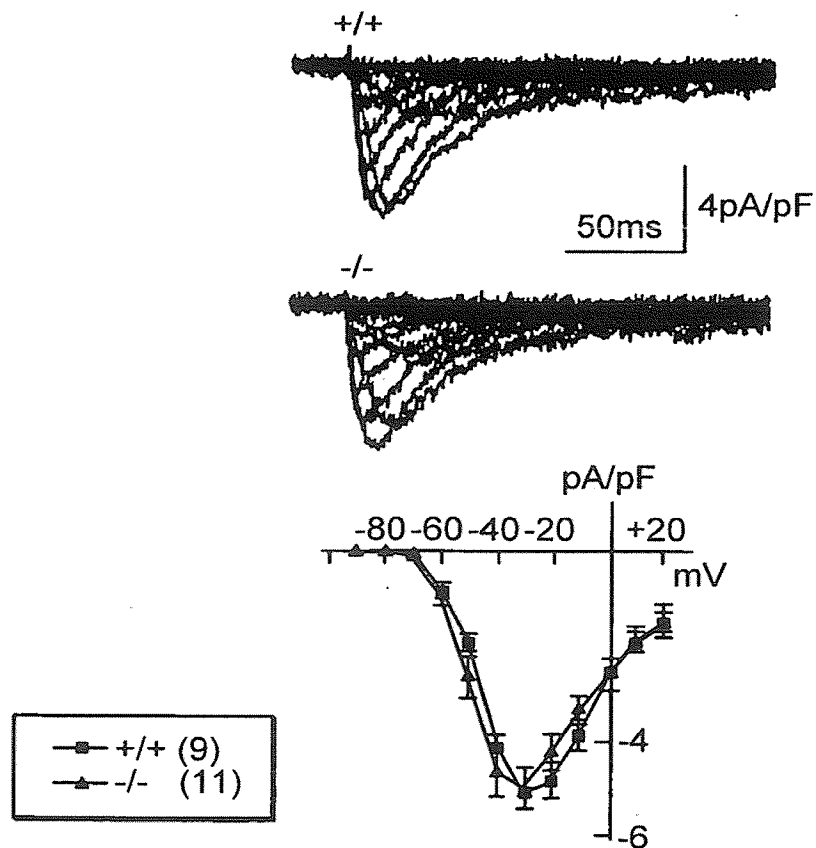


FIG. 3D

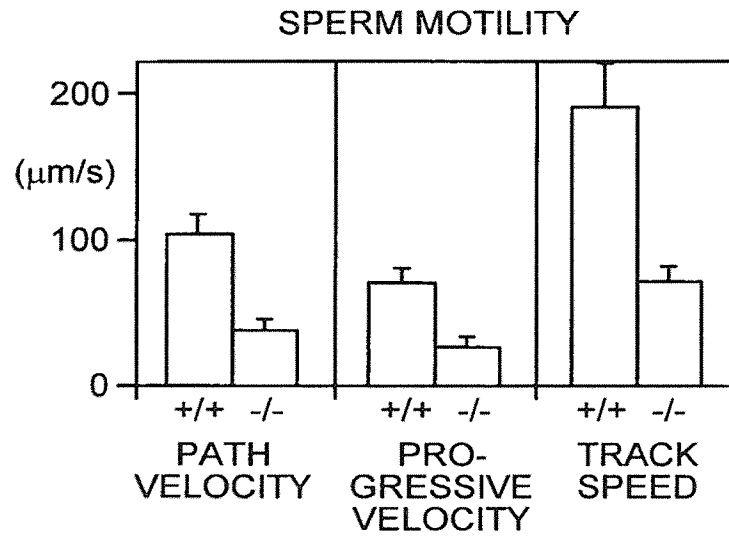


FIG. 4A

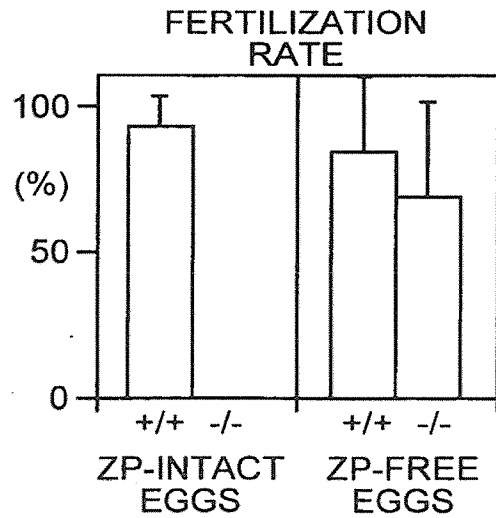


FIG. 4B

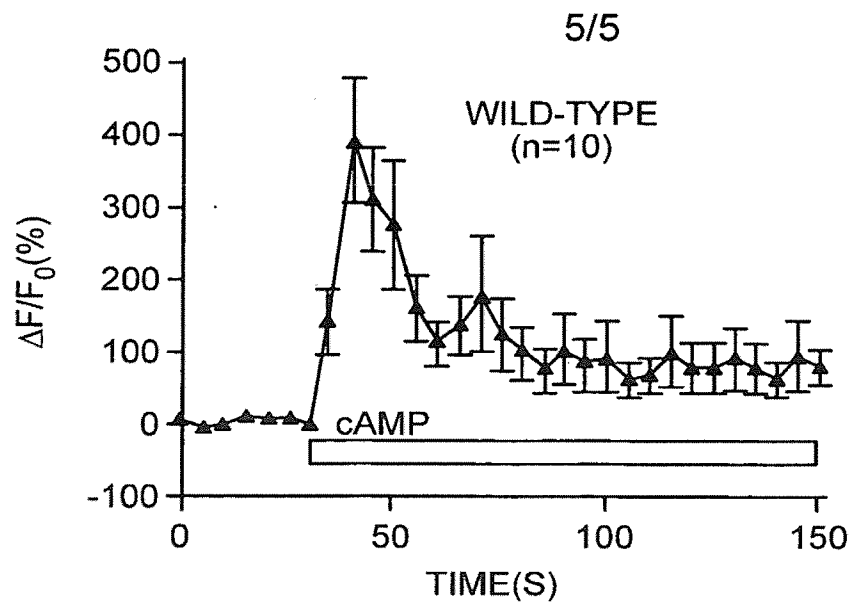


FIG. 5A-1

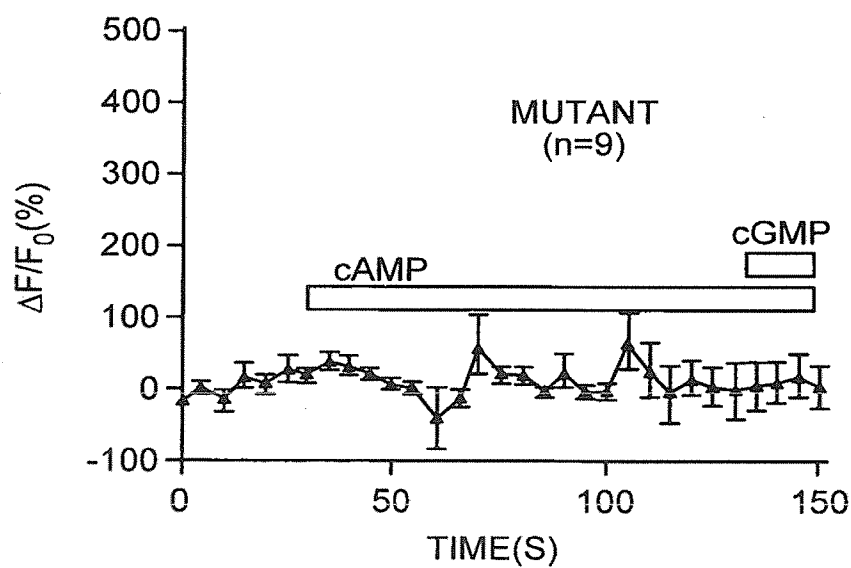


FIG. 5A-2

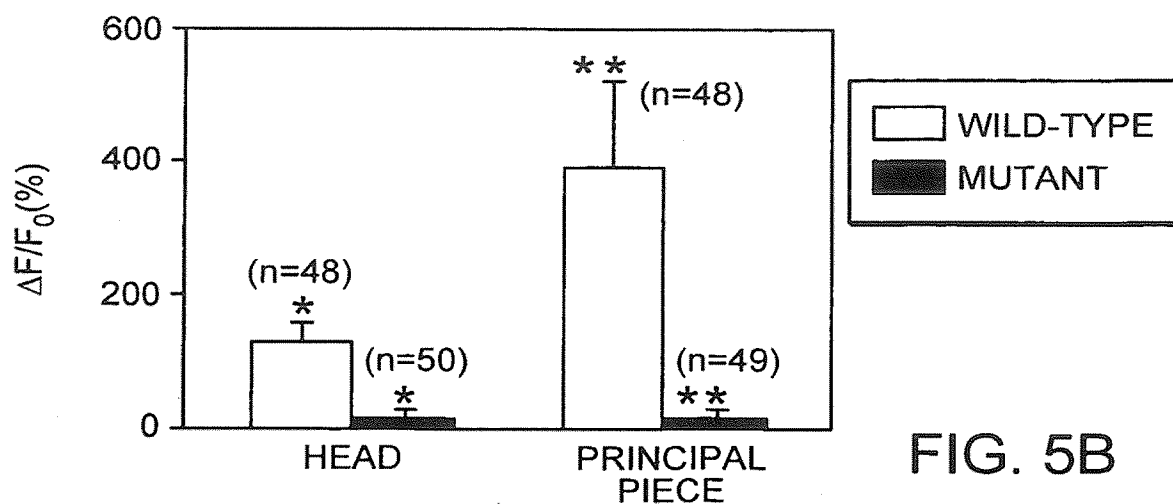


FIG. 5B